

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 18, 2002, 05:11:43 ; Search time 116.57 Seconds
(without alignments)
390.303 Million cell updates/sec

Title: US-09-719-748-2_COPY_13_275

Perfect score: 1343
Sequence: 1 YDIGEELGSGQFATVKKCRE.....LVKETRKRLTQEAALRHPWT 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 56222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SPTREMBL_19,*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriapl:*
- 17: sp_archeapl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

RESULT		1				
ID	075892	PRELIMINARY;	PRT; 370 AA.			
AC	075892;					
DT	01-NOV-1998	(TREMBLrel. 08, Created)				
DT	01-NOV-1998	(TREMBLrel. 08, Last sequence update)				
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)				
DE	DAP-KINASE RELATED PROTEIN 1.					
Homo sapiens (Human).						
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;						
NCBL-TAXID=9606; [1]						
RP	SEQUENCE FROM N.A.					
RC	TISSUE=KIDNEY;					
RX	MEDLINE=20094963; PubMed=10629061;					
RA	Inbal B., Shani G., Cohen O., Kissil J.L., Kimchi A.;					
RT	"Death-associated protein kinase-related protein 1, a novel Serine/threonine kinase involved in apoptosis.";					
RT	Mol. Cell. Biol. 20:1044-1054(2000).					
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.					
DR	EMBL; AF052941; ARJ3501.1; -.					
DR	HSSP: Q63450; 1A06.					
DR	InterPro; IPR00719; Euk_pk kinase.					
DR	InterPro; IPR002290; Ser-thr_pk kinase.					
DR	Pfam; PF00069; pk kinase; 1.					
DR	SMART; SM00220; S_TKC; 1.					
DR	PROSITE; PS0107; PROTEIN_KINASE_ATP; 1.					
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.					
DR	PROSITE; PS0108; PROTEIN_KINASE_ST; 1.					
KW	ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.					
SEQUENCE	370 AA; 42923 MW; 09502B4ANDCD20F91 CRC64;					
QY	9933e7 mus musculus Q91x59 cavia porcellus Q961u1 drosophila Q9V4F7 drosophila Q76381 drosophila Q16980 drosophila Q96dv1 homo sapiens Q23260 cenorhabditis Q95s19 drosophila Q01651 drosophila Q9gv81 drosophila Q9gv79 drosophila Q01653 drosophila Q23550 cenorhabditis Q23551 cenorhabditis Q9V4S5 homo sapiens Q91fl1 rattus norvegicus Q91r3 homo sapiens Q01652 drosophila Q23550 cenorhabditis Q23551 cenorhabditis Q61269 mytilus galloprovincialis Q9gv22 mytilus galloprovincialis Q15598 homo sapiens Q10466 homo sapiens Q97754 tryctolagus Q9gv80 drosophila Q9gvx9 drosophila Q91lqr4 arabidopsis					

ALIGNMENTS	
Query	Match
99.2%	Score 1332; DB 4; Length 370;
99.6%	Pred. No. 1.5e-95;
0;	Mismatches 1; Indels 0; Gaps 0;
1;	
99.6%	Best Local Similarity
99.6%	Matches 262; Conservative 0;
0;	Mismatches 1; Indels 0; Gaps 0;
0;	
99.6%	Query 1 YDIGEELGSGQFATVKKCREKSTGLEYAAFKFIKKRROSASRRGVSVREIEREVSIROYL 60
99.6%	99.4% 11 091x59
99.4%	091x58 rattus norvegicus

RESULT	4	DE	2310039H24RIK PROTEIN (FRAGMENT).
Q9JUP7	PRELIMINARY;	PRT;	1430 AA.
ID	09JUP7;	PR	1430 AA.
AC	09JUP7;	OS	Mus musculus (Mouse).
DT	01-OCT-2000 (TREMBrel. 15, Created)	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DT	01-OCT-2001 (TREMBrel. 19, Last sequence update)	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
DE	DEATH ASSOCIATED PROTEIN KINASE.	OX	NCBI_TAXID=10090;
OS	Mus musculus (Mouse).	RN	[1]
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RP	SEQUENCE FROM N.A.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;	RC	STRAIN=C57BL/6J; TISSUE=TONGUE;
OX	NCBI_TAXID=10090;	RX	MEDLINE=2108560; PubMed=1127851;
RN	[1]	RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RR	SEQUENCE FROM N.A.	RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RC	TISSUE=BRAIN;	RA	Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
RA	Kimchi A.;	RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa S., Clasavant T.,
RA	RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.	RA	Kadota K., Matsuda H.A., Ashburner M., Battalov S., Clasavant T.,
RA	-1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA	EMBL: X9048; CA65762.1. -.	RA	Kuehl P., Lewis S., Matsuo Y., Nishida I., Pesole G., Quackenbush J.,
DR	EMBL: X9048; CA65762.1. -.	RA	Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
DR	PFam: PF00023; ank; 8.	RA	Sasaki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
DR	SMART: SM00246; ANK; 8.	RA	Blake J., Boffelli D., Bojunga N., Carrinchi P., de Bonaldo M.F.,
DR	SMART: SM00005; DEATH; 1.	RA	Brownstein M.J., Bult C., Fleicher C., Fujita M., Garibaldi M.,
DR	SMART: SM00220; S_TKC; 1.	RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
DR	PROSITE: PS50088; ANK_REPEAT; 7.	RA	Lions P., Marchionni L., Mashima T., Mazzarelli J., Mombaerts P.,
DR	PROSITE: PS50297; ANK_REPEAT; 1.	RA	Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
DR	PROSITE: PS50017; DEATH_DOMAIN; 1.	RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
DR	PROSITE: PS50017; PROTEIN_KINASE_ATP; 1.	RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilkinson L.,
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.	RA	Wynshaw-Boris A., Yoshida K., Hasagawa Y., Kawaji H., Kohtsuki S.,
DR	PROSITE: PS50018; PROTEIN_KINASE_ST; 1.	RA	Hayashizaki Y.;
KW	ANK repeat; ATP-binding; Kinase; Repeat; Serine/threonine-protein kinase; kinase; transferase.	RT	"Functional annotation of a full-length mouse cDNA collection.";
SO	SEQUENCE 1430 AA; 159843 MW; 81C8356CDD14BBEB CRC64;	RL	Nature 409:685-690 (2001);
Query	Match	DE	DR
Query	Best Local Similarity 84.0%; Score 1128; DB 11; Length 1430; Matches 211; Conservative 37; Mismatches 15; Indels 0; Gaps 0;	GN	EMBL: AK009701; BAB26448.1. -.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	GN	DR
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	HSPP	063450; TA06.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	MGD	MGI:1916885; 2310039H24RIK.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	InterPro: IPR000719; Euk_Pkinase.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	InterPro: IPR002290; Ser-thr_Pkinase.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	InterPro: IPR001245; Tyr_Pkinase.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	PFam: PF00069; Pkinase; 1.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	PRINTS; PR00109; TYRKINASE.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	SMART; SM00220; S_TKC; 1.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	SMART; SM0019; TYRK; 1.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	PROSITE; PS500107; PROTEIN_KINASE_ATP; 1.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	KW ATP-binding; transferase.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	FT	FT
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	SEQUENCE	SEQUENCE 345 AA; 39776 MW; F7D1B4F71CA39C0 CRC64;
Query	Match	DE	2310039H24RIK PROTEIN (FRAGMENT).
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	GN	2310039H24RIK.
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	OS	Mus musculus (Mouse).
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	OX	NCBI_TAXID=10090;
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RN	[1]
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RP	SEQUENCE FROM N.A.
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RC	STRAIN=C57BL/6J; TISSUE=TONGUE;
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RX	MEDLINE=2108560; PubMed=1127851;
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa S., Clasavant T.,
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Kadota K., Matsuda H.A., Ashburner M., Battalov S., Clasavant T.,
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Kuehl P., Lewis S., Matsuo Y., Nishida I., Pesole G., Quackenbush J.,
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Sasaki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Blake J., Boffelli D., Bojunga N., Carrinchi P., de Bonaldo M.F.,
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Brownstein M.J., Bult C., Fleicher C., Fujita M., Garibaldi M.,
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Lions P., Marchionni L., Mashima T., Mazzarelli J., Mombaerts P.,
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilkinson L.,
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Wynshaw-Boris A., Yoshida K., Hasagawa Y., Kawaji H., Kohtsuki S.,
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RA	Hayashizaki Y.;
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RT	"Functional annotation of a full-length mouse cDNA collection.";
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	RL	Nature 409:685-690 (2001);
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR EMBL: AK009701; BAB26448.1. -.
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR HSSP: 063450; TA06.
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR MGD: MGI:1916885; 2310039H24RIK.
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR InterPro: IPR000719; Euk_Pkinase.
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR InterPro: IPR002290; Ser-thr_Pkinase.
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR InterPro: IPR001245; Tyr_Pkinase.
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR PFam: PF00069; Pkinase; 1.
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR PRINTS; PR00109; TYRKINASE.
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR SMART; SM00220; S_TKC; 1.
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR SMART; SM0019; TYRK; 1.
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR PROSITE; PS500107; PROTEIN_KINASE_ATP; 1.
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	DR	KW ATP-binding; transferase.
Db	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	FT	FT
Qy	61 HHNVTLLDYENRTDVHLLVLEVGGEFLDFAKQESLSEEEATSPKQIQLDGVNLYHT 120	SEQUENCE	SEQUENCE 345 AA; 39776 MW; F7D1B4F71CA39C0 CRC64;
Query	Match	DE	2310039H24RIK PROTEIN (FRAGMENT).
Qy	Best Local Similarity 83.8%; Score 1125; DB 11; Length 345; Matches 210; Conservative 38; Mismatches 15; Indels 0; Gaps 0;	GN	2310039H24RIK.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	OS	Mus musculus (Mouse).
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	OX	NCBI_TAXID=10090;
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RN	[1]
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RP	SEQUENCE FROM N.A.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RC	STRAIN=C57BL/6J; TISSUE=TONGUE;
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RX	MEDLINE=2108560; PubMed=1127851;
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Aizawa K., Iizawa M., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa S., Clasavant T.,
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Kadota K., Matsuda H.A., Ashburner M., Battalov S., Clasavant T.,
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Kuehl P., Lewis S., Matsuo Y., Nishida I., Pesole G., Quackenbush J.,
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Schrinl L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Sasaki K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Blake J., Boffelli D., Bojunga N., Carrinchi P., de Bonaldo M.F.,
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Brownstein M.J., Bult C., Fleicher C., Fujita M., Garibaldi M.,
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Lions P., Marchionni L., Mashima T., Mazzarelli J., Mombaerts P.,
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Nordone P., Ring B., Ringwald M., Rodriguez T., Sakamoto N.,
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilkinson L.,
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Wynshaw-Boris A., Yoshida K., Hasagawa Y., Kawaji H., Kohtsuki S.,
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RA	Hayashizaki Y.;
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RT	"Functional annotation of a full-length mouse cDNA collection.";
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	RL	Nature 409:685-690 (2001);
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR EMBL: AK009701; BAB26448.1. -.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR HSSP: 063450; TA06.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR MGD: MGI:1916885; 2310039H24RIK.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR InterPro: IPR000719; Euk_Pkinase.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR InterPro: IPR002290; Ser-thr_Pkinase.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR InterPro: IPR001245; Tyr_Pkinase.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR PFam: PF00069; Pkinase; 1.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR PRINTS; PR00109; TYRKINASE.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR SMART; SM00220; S_TKC; 1.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR SMART; SM0019; TYRK; 1.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR PROSITE; PS500107; PROTEIN_KINASE_ATP; 1.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	DR	KW ATP-binding; transferase.
Db	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	FT	FT
Qy	YD1GIGELGSQFAVKKCCKSTGLEYAKFKKRQSRASRRGVSREELERYEVSILRQL 60	SEQUENCE	SEQUENCE 345 AA; 39776 MW; F7D1B4F71CA39C0 CRC64;
Query	Match	DE	2310039H24RIK PROTEIN (FRAGMENT).
Qy	Best Local Similarity 83.8%; Score 1125; DB 11; Length 345; Matches 210; Conservative 38; Mismatches 15; Indels 0; Gaps 0;	GN</	

OBBL8 PRELIMINARY; PRT; 367 AA.
 ID OBBL8; PRELIMINARY; PRT; 367 AA.
 AC OBBL8;
 DT 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE SIMILAR TO DEATH-ASSOCIATED PROTEIN KINASE 1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP TISSUE-MELANOMA;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 CC -I SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; BC00514; AAH03614.1; -.
 DR HSSP; 063450; 1A06.
 DR InterPro; IPR002290; Ser_Thr_Pkinase.
 DR InterPro; IPR00245; Tyr_Pkinase.
 DR Pfam; PF0069; Pkinase; 1.
 DR PRINTS; PRO019; TIRKINASE.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding, Kinase; Serine/threonine-protein kinase; transferase.
 SQ SEQUENCE 367 AA; 42115 MW; 42ED1DE7191FE3FD CRC64;

Query Match 83.7%; Score 1124; DB 4; Length 367;
 Best Local Similarity 79.5%; Pred. No. 2.1e-79; Mismatches 13; Indels 0; Gaps 0;
 Matches 209; Conservative 41; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YDIGERGLSGOFATYKKCREKSTGLEYAAKFKKKRQSARSGRRGSREELREVSTLQVL 60
 Db 13 YDGEELGLSGOFATYKKCREKSTGLEYAAKFKKKRQSARSGRRGSREELREVSTLQVL 60
 Qy 61 HHNVTLHDYENRDTWHLLELVSGLGELDFLACKESLSEEATSFQIKOILDGVNLHT 120
 Db 73 HPNITLHDYENRDTWHLLELVSGLGELDFLACKESLSEEATSFQIKOILDGVNLHT 120
 Qy 121 KKIAHFDLKPEINIMLDKKNIPHIKLIDGLAHEDVEFKNFGTPEFVABIVNVE 180
 Db 133 LQIAHFDLKPEINIMLDKKNIPHIKLIDGLAHEDVEFKNFGTPEFVABIVNVE 192
 Db 73 HPNITLHDYENRDTWHLLELVSGLGELDFLACKESLSEEATSFQIKOILDGVNLHT 132
 Qy 181 PLGLEADMWSIGVITYILSGASPFGLDKQETANITSVSYDDEEFFSHTSELAKDFI 240
 Qy 121 KKIAHFDLKPEINIMLDKKNIPHIKLIDGLAHEDVEFKNFGTPEFVABIVNVE 180
 Db 193 PLGLEADMWSIGVITYILSGASPFGLDKQETANITSVSYDDEEFFSHTSELAKDFI 252
 Qy 241 RKLLVKETRKRLTQEARLHPIWI 263
 Db 253 RRLLVKDPKRRMTIAQSLEHWSI 275

RESULT 7
 ID 043293 PRELIMINARY; PRT; 454 AA.
 AC 043293
 DT 01-JUN-1998 (TREMBrel. 06, Created)
 DT 01-JUN-1998 (TREMBrel. 06, Last sequence update)
 DT 01-OCT-2001 (TREMBrel. 18, Last annotation update)
 DE ZIP-KINASE.
 GN ZIP-KINASE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP

OBBL8 PRELIMINARY; PRT; 448 AA.
 ID OBBL8; PRELIMINARY; PRT; 448 AA.
 AC OBBL8;
 DT 01-JUN-1998 (TREMBrel. 06, Created)
 DT 01-JUN-1998 (TREMBrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE ZIP-KINASE.
 GN DAPK3.
 OS Mus musculus (Mouse).
 OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TAXID=10090;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=98147805; PubMed=9488481;
 RX Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;
 RA "ZIP kinase, a novel serine/threonine kinase which mediates
 RT "ZIP kinase, a novel serine/threonine kinase which mediates
 RT "ZIP kinase, a novel serine/threonine kinase which mediates
 RT Mol. Cell. Biol. 18:1642-1651(1998).
 RL [2] SEQUENCE FROM N.A.
 RX MEDLINE=99383879; PubMed=10356987;
 RA Murata-Hori M., Suizu F., Iwasaki T., Kikuchi A., Hosoya H.;
 RT "ZIP kinase identified as a novel myosin regulatory light chain kinase
 RT in HeLa cells.";
 RL FEB5 Lett. 451:81-84(1999).
 CC -I SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; AB001144; BAA2495.1; -.
 DR HSSP; 063450; 1A06.
 DR InterPro; IPR000719; Ser_Thr_Pkinase.
 DR InterPro; IPR002290; Ser_Thr_Pkinase.
 DR Pfam; PF0069; Pkinase; 1.
 DR PRINTS; PRO019; TIRKINASE.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; transferase.
 SQ SEQUENCE 454 AA; 52535 MW; 567730086A6A1CF0 CRC64;

Query Match 83.5%; Score 1121; DB 4; Length 454;
 Best Local Similarity 79.8%; Pred. No. 4.7e-19; Mismatches 17; Indels 0; Gaps 0;
 Matches 210; Conservative 36; Mismatches 17; Indels 0; Gaps 0;

Qy 1 YDGEELGLSGOFATYKKCREKSTGLEYAAKFKKKRQSARSGRRGSREELREVSTLQVL 60
 Db 13 YDGEELGLSGOFATYKKCREKSTGLEYAAKFKKKRQSARSGRRGSREELREVSTLQVL 60
 Qy 61 HHNVTLHDYENRDTWHLLELVSGLGELDFLACKESLSEEATSFQIKOILDGVNLHT 120
 Db 73 HPNITLHDYENRDTWHLLELVSGLGELDFLACKESLSEEATSFQIKOILDGVNLHT 120
 Qy 121 KKIAHFDLKPEINIMLDKKNIPHIKLIDGLAHEDVEFKNFGTPEFVABIVNVE 180
 Db 133 LQIAHFDLKPEINIMLDKKNIPHIKLIDGLAHEDVEFKNFGTPEFVABIVNVE 192
 Db 73 HPNITLHDYENRDTWHLLELVSGLGELDFLACKESLSEEATSFQIKOILDGVNLHT 132
 Qy 181 PLGLEADMWSIGVITYILSGASPFGLDKQETANITSVSYDDEEFFSHTSELAKDFI 240
 Qy 121 KKIAHFDLKPEINIMLDKKNIPHIKLIDGLAHEDVEFKNFGTPEFVABIVNVE 180
 Db 193 PLGLEADMWSIGVITYILSGASPFGLDKQETANITSVSYDDEEFFSHTSELAKDFI 252
 Qy 241 RKLLVKETRKRLTQEARLHPIWI 263
 Db 253 RRLLVKDPKRRMTIAQSLEHWSI 275

RESULT 8
 ID 054784 PRELIMINARY; PRT; 448 AA.
 AC 054784;
 DT 01-JUN-1998 (TREMBrel. 06, Created)
 DT 01-JUN-1998 (TREMBrel. 06, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE ZIP-KINASE.
 GN DAPK3.
 OS Mus musculus (Mouse).
 OC Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TAXID=10090;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=8147805; PubMed=9488481;
 RX Kawai T., Matsumoto M., Takeda K., Sanjo H., Akira S.;
 RA "ZIP kinase, a novel serine/threonine kinase which mediates
 RT "ZIP kinase, a novel serine/threonine kinase which mediates
 RT "ZIP kinase, a novel serine/threonine kinase which mediates
 RT Mol. Cell. Biol. 18:1642-1651(1998).
 RL

RESULT: 15
 Q88850 PRELIMINARY; PRT; 907 AA.
 ID Q88850;
 AC 08850;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE NEURONAL MYOSIN LIGHT CHAIN KINASE 1.
 GN GMCLCK1.
 OS *Carassius auratus* (Goldfish).
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cyprinidae; Cyprinidae; Carassius.
 OX NCBI_TaxID:7957;
 RN [1]
 RP SEQUENCE FROM N.A.
 RG STRAIN=COMMON COMET;
 RK MEDLINE=97067382; PubMed=9910795;
 RA Jian X., Scaro B.G., Schmidt J.T.;
 RT "Myosin light chain kinase: expression in neurons and upregulation
 during axon regeneration.";
 RL J. Neurobiol. 31:379-391(1996).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; US1731; ARB41402.1; -.
 DR HSSP; P56276; ITRK.
 DR InterPro; IPR000719; Euk_Pkinase.
 DR InterPro; IPR033961; FN_TII.
 DR InterPro; IPR003598; Ig_C2.
 DR InterPro; IPR00006; Ig_MIC.
 DR InterPro; IPR002290; Ser_Thr_Pkinase.
 DR Pfam; PF00041; In3; 1.
 DR Pfam; PF00047; Ig; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR SMART; SM00060; FN3; 1.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Immunoglobulin domain; Kinase;
 KW Serine/threonine-protein kinase; Transf erase;
 SQ SEQUENCE 907 AA; 101423 MW; 386BA3BP31362C CRC64;

Query Match 47.4%; Score 636.5; DB 13; Length 907;
 Best Local Similarity 45.8%; Pred. No. 4.8e-41; Mismatches 121; Conservative 56; Indels 9; Gaps 3; Matches 121; Conservative 56; Mismatches 78; Indels 9; Gaps 3;

Qy 1 YDIDGEELGSQFATWKKCREEKSTGLEYAAKFKKKRQSRASRRGVSYRGSREELREVSTLRLQVL 60
 Db 470 YDVEDRLGTCGKFQAVFKLKLTKWAGKFKIAYSAK----EKDNVQREAIWMDR 523
 Qy 61 HHNVTLDHVYENRTDVHVTLELVSGGELFDPLAQKE-SLSEERATSFKQIOLGVNVLH 119
 Db 524 HPKLVQCVDAFEGKIDIVMYLEMVGSGELPERIADDEFELTERREVIKYMLQIVDGVSFH 583
 Qy 120 TKGTAHFDLKPPENIMLDDKIPPIPHKLIDFGAHEIEGVFERNIFGPEFVAPENVY 179
 Db 584 KKGIVHDLKPPENIMCWNKTT-GSKRKLIDFGARRLENAGSLKVLEGTPPEFVAPENVY 641
 Qy 180 EPLGIEADWMSIGVITYILISGASPFLGDTQETANITSVSVDDEEFSHTSSELAKDF 239
 Db 642 EAISYATDMSIVGIVCYTIVSGLSPFMGNDNDETLNSVATWDFEDEAFDEISDEAKDF 701
 Qy 240 ITRKLIVKETTRKLRTQEAALRHPWI 263
 Db 702 ISNLUKKDMKARLSCDQCFQHPWL 725

This Page Blank (USP10)